Simulation of Impacts of Annosus Root Disease with the Western Root Disease Model[1]

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Abstract: The Western Root Disease Model as it currently exists is described, and the assumptions that were made to adapt the model to simulate attack by Heterobasidion annosum in coniferous forests of south-central Oregon are defined. Some simulations produced by this adapted model are presented to stimulate provocative discussion, thought, and action. These simulations indicate that with no action, or with continued improper management, annosus root disease will severely reduce timber yields in affected stands of true fir. Coupled with other information, this exercise provides a framework from which to build an annosus variant of the Western Root Disease Model.

HISTORY AND BACKGROUND

Tree root diseases occur on most forested lands in North America. Timber losses in the western United States alone are estimated at some 240 million cubic feet annually (Smith 1984). The most damaging tree root pathogens in the West are: pathogenic species of Armillaria; Phellinus weirii (Murr.) Gilbn.; and Heterobasidion annosum (Fr.) Bref.

Recognizing the seriousness of this economic loss, the USDA Forest Service initiated a project to develop a root disease model for use in silvicultural planning and management in western coniferous forests (Brookes 1985, McNarnee and others 1989, Stage and others 1989, Eav and Shaw 1987, Shaw and others 1985). At present, all actions in the model that are dictated by disease behavior can represent either pathogenic species of Armillaria (Wargo and Shaw 1985) or P. weirii (Thies 1984). Possibilities for further adaptation of this model to include several root diseases in the same stand or root diseases that spread by airborne propagules as well as through roots, as with H. annosum, were beyond the initial scope of the project.

In this paper, the Western Root Disease Model as it currently exists is described, and the assumptions that were made to adapt the model to simulate attack by H. annosum in coniferous forests of south-central Oregon are defined. Some of the simulations produced by this adapted model are presented to stimulate provocative discussion, thought, and action.

We are aware of two other models that simulate the effects of H. annosum on stand development and harvestable tree volumes (Alexander and others 1985, Pratt and others 1989). Neither of these models, however, appeared to be adaptable to annosus root disease in the West because they deal with plantations containing a single tree species, whereas forest conditions in the West frequently represent an array of management strategies applied in multi-storied, multi-species, and multi-aged stands of varying densities.

Structure of the Western Root Disease Model

The Western Root Disease Model consists of three main components: the root disease submodel, an "other agents" submodel, and a stand interface submodel. The root disease submodel considers the status and spread of root disease. The "other agents" submodel simulates the effects of wind-throw and three types of bark beetle behavior. This submodel is important because it provides a structure for considering the interactions between root diseases and other damaging agents. The stand interface submodel provides the interaction between the stand growth model to which the Western Root Disease Model must be attached, currently Prognosis (Wykoff and others 1982, Stage 1973), and the root disease and "other agents" submodels.

At present, the model provides a dynamic representation of the spatial and temporal

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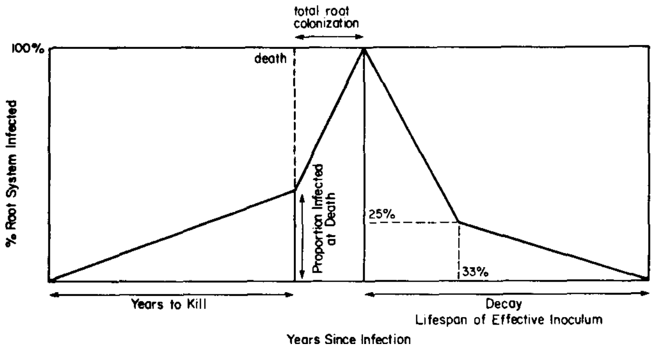

Figure 1--Pattern of root pathogen spread and inoculum buildup and decline in a single tree root system.

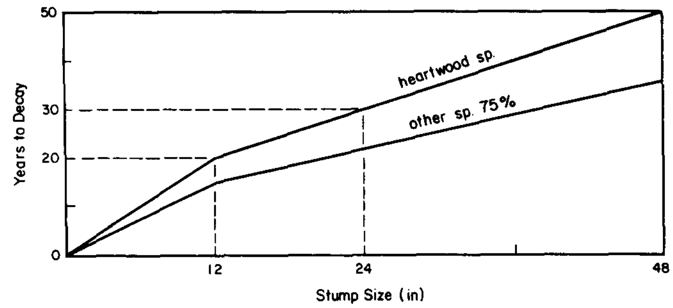

Figure 3--Lifespan of inoculum for various tree species infected with Armillaria; see text for detailed description.

epidemiology of pathogenic species of Armillaria or P. weirii. The primary assumption for the model is that the distribution of root disease within a stand can be characterized by a number of spreading root disease centers, each of which contains infected trees, noninfected trees, and other inoculum sources (i.e., infected stumps). The disease centers are defined by their locations in the stand (coordinates) and their size (radii).

Three important characteristics of root disease centers are addressed: the dynamics of infection and inoculum within root disease centers; the expansion rate of spreading root disease centers; and the carry-over of root disease to a new stand following a clearcut.

Before characterizing the spread of root disease centers through a stand, we must describe disease spread through the roots of individual trees. Figure 1 depicts how live root systems become infected, how trees are killed, and how infection spreads in roots. In the model, the quantity of inoculum is measured as area occupied by infected roots since this quantity is directly related to the probability of root contact.

The time necessary to kill a Douglas-fir (Pseudotsuga menziesii (Mirb.) Franco) tree on Douglas-fir habitat in the interior region of the western United States is defined by the relationship shown in Figure 2. This relationship is modified for other species, pathogens, and habitat types, as shown in the figure, but the assumption is that all trees react similarly to infection. In the current model, variations between habitat types can be accommodated by using the appropriate Keywords to change parameter values (see below).

The average portion of a root system that is colonized by the pathogen when a tree dies is a function of the pathogen species and tree species (Table 1). Following tree death, the progress of disease depends on the pathogen; Armillaria species colonize the entire root system within 5 years. For P. weirii, the proportion of infected roots does not increase after tree death. For both pathogens, inoculum is assumed to deteriorate rather rapidly after its maximum buildup. The lifespan of effective inoculum is a function of stump size and tree species (Figure 3). Tree species are grouped into heartwood and nonheartwood types. Species with heartwood include Douglas-fir, ponderosa pine (Pinus ponderosa Dougl. ex Laws.), white pine (P. monticola Dougl. ex D. Don), sugar pine (P. lambertiana Dougl.), lodgepole pine (P. contorta var. latifolia Engelm.), western red cedar (Thuja plicata Donn ex D. Don), and western larch (Larix occidentalis Nutt.); nonheartwood species include white fir (Abies concolor (Cord. and Glend.) Lindl. ex Hildebr.),

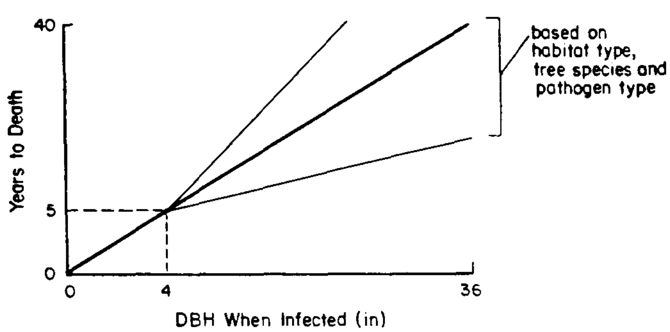

Figure 2--Time required from infection by Armillaria to tree death for Douglas-fir on a Douglas-fir habitat type.

Table 1--Average percentage of root systems assumed to be infected at the time a tree is killed by root disease

Tree species	Fungal Species	
	Armillaria	P. weirii
	(pct root system infected)	
Douglas-fir	80	60
Pines	30	85
True fir	80	60
Hemlock	80	80
Spruce	75	65
Larch	85	75
Cedar	75	85

grand fir (A. grandis (Dougl. ex D. Don) Lindl.), western hemlock (Tsuga heterophylla (Raf.) Sarg.), and Engelmann spruce (Picea engelmannii Parry ex Engelm).

Inoculum is assumed to decay at a rate that reduces the radial extent of infected root systems by 75 percent during the first one-third of their lifespan. The remaining infected roots are assumed to decay at a steady rate over the remaining two-thirds of their lifespan.

Simulation of root disease dynamics

The simulation for enlargement of infection centers has three main components: an estimation of the average rate of enlargement; the translation of that rate into an area of stand newly encompassed by root disease; and translation of that area into the number of trees newly infected.

How root disease centers are affected by clearcutting and regeneration of a new stand is poorly understood. The model considers three different scenarios: root disease centers from the former stand cease to exist after clearcutting, and root disease in the new stand arises in a small number of new centers located within previously infected areas; root disease centers from the former stand retain their integrity, and, as the new stand matures, these centers enlarge, starting at their old boundaries; and after a clearcut and regeneration, root disease centers form around certain individual pieces of inoculum throughout the area affected in the former stand and these centers gradually expand and coalesce. These three scenarios actually form a continuum that is dependent on the density of inoculum and the probability of a piece of inoculum initiating a new center that is capable of expanding.

REPRESENTATION OF MANAGEMENT ACTIONS

Direct Control of Root Disease

The Western Root Disease Model can implement only one management action specifically used for control of root disease, that of "pushing" or removing infected stumps and their root systems. This option can be requested in a specific year, with a factor specifying the efficiency with which roots are removed and the minimum diameter of dead trees and stumps to be removed. Even though this practice is an accepted management alternative in certain stands, it is not universally applicable (Wargo and Shaw 1985).

Silvicultural Treatments

The wide variety of silvicultural options available with the Prognosis growth and yield model (Wykoff and others 1982) can also be invoked to analyze alternative methods for control of root disease. Regeneration systems ranging from single-tree selections to clearcutting can be simulated. In addition to the harvest of existing trees, new stands can be introduced following site preparation either by natural regeneration or by planting. Of these, modification of species composition in regenerated stands (through planting or choice of regeneration systems) is the most effective means of avoiding future root disease problems.

A full range of treatment alternatives may be considered when regenerating diseased stands, depending on economic constraints and stand management objectives. The most frequent approach to management of root disease problems in timber stands is regeneration to site-suited tree species that are disease tolerant. The model can be used to compare the effects of variations of this approach with the effects of other approaches. For example, the following options may be compared and considered:

- A clearcut, seed tree cut, or shelterwood cut followed by regeneration to a disease-tolerant species, or to a mixed stand with a predominance of tolerant species.

- Overstory removal from an understory of tree species that might be disease susceptible, disease tolerant, or a mixture of the two.

- A clearcut and stump removal, followed by planting of a disease-susceptible, but otherwise preferred species.

- No action--leave the stand "as is", but recognize presence of root disease.

- Stand regeneration to a disease susceptible species without stump removal.

- A straight simulation, without invoking the Western Root Disease Model, of the Prognosis growth and yield model; perhaps followed by planting of a preferred, but disease susceptible, tree species. These scenarios represent "control" simulations for the Western Root Disease Model.

WHAT DATA ARE REQUIRED?

The model is designed to start with sample inventories of actual stands. For example, the compartment examination procedure described by Stage and Alley (1972) and in the Forest Service Handbook for Region 1 (USDA Forest Service 1986) can supply the necessary stand data if it is augmented to include stumps infected with root disease.

In addition to the customary tree size attributes, the model uses information on the frequency of tree infection by root disease pathogens. This value can be compiled by the model from disease status codes of the individual sample trees, or supplied by the user from an overall estimate based on an independent sample of the stand. The Western Root Disease Model also uses data on the area of the stand and the sizes and distribution of disease centers to initiate the simulation. The model can start from bare ground by invoking the Regeneration/Establishment component of Prognosis (Ferguson and Crookston 1984), or from the stand description contained in the list of trees sampled in the inventory. Proportions of trees infected and proportions of roots infected within diseased areas can be supplied in the aggregate, or by specifying the disease status of each tree in the sample inventory.

KEYWORDS

The Western Root Disease Model is controlled, and its parameter values are modified, by 26 Keywords (Stage and others 1989) that are similar in structure and use to those in the Prognosis Keyword System (Wykoff and others 1982). To invoke the Western Root Disease Model, a sequence of its Keywords are inserted into the sequence of Prognosis Keywords through the Pest Model Submittal System (Gladden 1989). Users of the Data General Growth and Yield Submittal System of the USDA Forest Service (Sleavin 1989) can access the Pest Model Submittal System by selecting the Keyword "PEST" from the Keyword Main Entry Menu. The Western Root Disease Model Keywords allow users to:

1. Control program execution, including the nature of root disease processes simulated, and the interactions with other agents.
2. Describe initial conditions of the stand and its disease status.
3. Specify the management prescriptions to be invoked.
4. Change critical parameters, particularly those which can be either habitat specific or dependent on the source of new trees, and to assume static rates and probabilities for one or more of the processes governing root disease dynamics.
5. Investigate the effects of bark beetles and windthrow on root disease dynamics.

To simulate attack by _H_. _annosum_, we worked primarily through this Keyword system, as described later.

CHARACTERISTICS OF ANNOSUS ROOT DISEASE IN SOUTH-CENTRAL OREGON

In south-central Oregon the Western Root Disease Model is used with the SORNEC variant of Prognosis (Johnson and others 1986). The following characteristics of root disease caused by _H. annosum_ were considered important to this exercise in modeling the dynamics of annosus root disease.

1) Long-distance spread of the pathogen is by windborne spores that land on, germinate on, and colonize wounds or freshly cut stump surfaces. The latter are particularly important. Infection foci develop almost exclusively in trees that surround large, infected stumps of the same species or type (i.e., true firs around true fir stumps and pines around pine stumps) that are 18 inches or more in diameter. The proportion of stumps that act as infection foci is related to past cutting history. Surveys (Filip and Goheen 1982, 1984) suggest that, in general, 25 percent of the large stumps created in the first harvesting entry in a susceptible host stand become infection foci and 50 percent of the large stumps created in subsequent entries become infection foci. The distribution of newly infected stumps in a stand appears to be essentially random, although to some unknown degree it is probably influenced by wind patterns.

   Once the pathogen is established, at least in true firs, it spreads via root grafts and contacts to adjacent hosts at a rate very similar to that of _P. weirii_--approximately 1 foot per year. With pines, the rate of spread is similar, but mortality centers develop mainly within the rooting zone of old infected pine stumps. Thus, the fungus appears to spread at about 1 foot per year on the root systems of old infected pine stumps, but does not spread much from live tree to live tree in the new stand.

2) Inoculum buildup and decline for _H. annosum_ differs from that currently modeled for pathogenic species of _Armillaria_ in the following ways:
   a) _H_. _annosum_ invades and colonizes uninfected, dead root systems. This invasion may include colonization through root contacts as well as by spores on stump surfaces. For this exercise, however, we assumed that the above-mentioned percentages of stumps that become infected following stand harvest entries capture both of these actions.
   b) The rate of root colonization on an infected tree is the same before and after tree death.
   c) The minimum length of survival time for active inoculum is 20 years--the current default value for inoculum survival of _P_. _weirii_.
   d) The rate of inoculum decay in the years after total root colonization appears to be slower for _H_. _annosum_ than for either pathogenic species of _Armillaria_ or _P_. _weirii_ (Fig. 3). This action and item b above were not adequately addressed in this

exercise because the default values for Armillaria were used. We do not, however, believe this difference to be serious.

3) Host susceptibility:
Very Susceptible--white fir, grand fir, ponderosa pine on very dry sites, and western juniper (Juniperus occidentalis Hook.) on sites where ponderosa pine is affected.
Less Susceptible--Douglas-fir, incense cedar (Librocedrus decurrens Torr.) in association with ponderosa pine, lodgepole pine, ponderosa pine (on all except very dry sites), sugar pine, white pine, and western larch.
In this geographic area, significant damage occurs exclusively in the very susceptible group. Infection of the less susceptible species may be more common than presently recognized, but mortality or noticeable tree decline is extremely rare.

4) Plant community type does not appear to influence development of annosus root disease on true firs. The significant factors with true firs seem to be the presence of large hosts and the stand's logging history. The disease is about equally severe on all habitat types in which true firs are a significant component of the stand and cutting has occurred. Plant community type is, however, a critical factor in identifying where annosus root disease will seriously affect ponderosa pine. Very dry habitat types are associated with damage. Indicator plants include western juniper, sagebrush (Artemisia tridentata Nutt.), bitterbrush (Purshia tridentata (Pursh) DC), wooly wyethia (Wyethia mollis A. Gray), serviceberry (Amelanchier sp.), Wheeler's bluegrass (Poa nervosa (Hook.) Vasey), fescue (Festuca sp.), and needle-grass (Stipa sp.).

5) White and grand firs are affected by the "S" type of H. annosum and ponderosa pine by the "P" type (Chase and others 1989). There appears to be little or no cross-over between pines and true firs as the fungal strains are rather host specific. For this exercise, we considered them to be specific which is why we indicated that trees become infected exclusively around stumps of the same species or type (i.e., true firs around true fir stumps).

6) Evidence suggests that infection centers caused by H. annosum, particularly in stands of true firs, retain their integrity through all stand entries.

7) If applied within 48 hours of cutting, borax treatment of stumps is over 95 percent effective in preventing surface infection by H. annosum (Graham 1971, Smith 1970).

8) Stump removal has not been tried as a control measure for annosus root disease on true firs in Oregon. It should be biologically effective if economically feasible. It is unlikely, however, that it would be used in other than unusual cases.

9) Regarding interactions with other agents, Scolytus ventralis LeConte commonly infests true fir infected by H. annosum, and Dendroctonus ponderosae Hopkins is common on infected ponderosa pine. We assume that at root infection levels of 30 percent, trees of either species could be killed by bark beetles (see INFKILL Keyword). Windthrow of infected trees is rather uncommon. Trees usually die standing and some years later break off rather than being windthrown. Trees infected by H. annosum are often infected by Armillaria spp. as well; however, that situation was ignored in this exercise.

STAND DESCRIPTION

For this exercise, we selected a 22 acre, 60-year-old stand located at an elevation of 3100 feet on the Deschutes National Forest. Current (1987) species composition (number of trees) is 89 percent white fir, 3 percent Douglas-fir, 3 percent ponderosa pine, and a 5 percent mixture of other conifers. These numbers are dominated by some 1625 white firs per acre that are ≤ 1 inch DBH which is why we indicated an understory removal in most of the simulations. The intent was to destroy these small trees, an action we felt would occur during logging activities designed to remove the overstory. This overstory removal coincident with destruction of the understory is considered to be a reasonable operational scenario for stands of this type in Eastside Oregon forests.

In terms of volume, the stand currently has 27,720 board feet per acre with 38 percent white fir, 28 percent ponderosa pine, 12 percent Douglas-fir, and 22 percent other species. This test stand is fairly typical of many mixed conifer stands on the Deschutes National Forest and is similar to stands on many other forests in the area as well.

Root disease is currently damaging in the stand and our initialization of infected area at 3.28 acres, as described below, probably under-represents current disease severity.

BRIEF DESCRIPTION OF KEYWORDS THAT WERE CRITICAL TO THE SIMULATION OF ANNOSUS ROOT DISEASE

Readers are referred to the User's Manual for the Western Root Disease Model (Stage and others 1989) for descriptions of all Keywords.

BBTYPE3--Specifies a Type 3 bark beetle event that kills trees infected by root disease. The user specifies a year and intensity to switch this agent on. The event will not occur before the specified cycle year and will not occur until the specified conditions are present. The Type 3 bark beetle routine is switched off after one outbreak has occurred. The description for Run 4B provides the defaults we used to simulate an attack by *S. ventralis* on true firs.

INFKILL--Specifies at what level of root infection trees die. Infection proceeds through a root system until a particular infection level is reached and then the tree dies. For this exercise, these values were set by tree species as follows:

WP	WL	DF	TF	C	LP	ES	PP[3]
.95	.95	.95	0.5	.95	.95	.95	1.0

INFMULT--Specifies infection probabilities for root disease contact and spread and allows the user to vary these probabilities for different tree species and sites. For this exercise, these values were set by tree species as follows:

WP	WL	DF	TF	C	LP	ES	PP[3]
.1	.1	.1	.6	.1	.1	.1	.1

INOCSPAN--Specifies the minimum life span of inoculum, in years, for each root disease type. That value was set at 20 years for this example.

RRIN--Used in the Prognosis simulation system to invoke the Western Root Disease Model.

RRINIT--Used when root disease conditions are initialized from user-supplied data (initialization is *not* directly from the input tree list). Indicates the area in root disease, and if known, the location of root disease centers. The user may specify a total area in root disease and the number of centers. In this case, the model randomly located root disease centers throughout the stand. Initially, each center will be of equal size, calculated as the total area in root disease divided by the number of centers. The alternative is to provide a list of root disease centers with X and Y coordinates and a radius for each center. This Keyword is mandatory and must be present.

For all simulations in this exercise we initialized the area of root disease at 3.28 acres equally distributed among 70 disease centers. These values were determined by hand calculating how many white firs •18 inches DBH were removed during the overstory removal of all trees •17 inches DBH. Based on the assumptions mentioned above, 25 percent (70) of these trees were destined to become infected by *H. annosum*. The equation in the model that calculates root extent based on tree diameter and species was extracted and used by hand to calculate the areas of root extent for these 70 trees; these areas totaled 3.28 acres.

RRJUMP--Specifies the extent, as measured in root system radii, to which root disease will expand outward from existing centers after a cut. The intent is to simulate disease spread through root systems on infected trees that are removed from around the edge of root disease centers when the stand is thinned or clearcut.

This Keyword became critical to completion of this exercise because it provided the only mechanism to increase the area of root disease in the stand after thinning. Based on the above-mentioned assumptions concerning annosus root disease in this geographic area, we calculated, as described for RRINIT, the area occupied by the root systems of 50 percent of the white firs •18 inches DBH that were removed in the first thinning. We then set RRJUMP at various levels and examined the root disease model output to see what level provided an area increase equal to what was calculated (about 4 acres). The value 0.5 provided the best estimate.

To allow use of this value required model reprogramming because in the current version of the Western Root Disease Model, RRJUMP could only be set as an integer value. We had to use 0.5 for the second thinning as well because, once initiated, we could not change the value for RRJUMP. We also could not change the number of centers, so the "new" area in root disease was added to the previous total and distributed randomly among the existing centers. This limitation did not greatly concern us because with 70 centers in 22 acres there is already a considerable degree of center overlap, a condition that the models captures, and increasing the number of centers would only increase this probability. This procedure was necessary because we could not stop and restart the base Prognosis model during the simulation to enter additional information on the status of root disease.

RRMINK: No differentiation was made for effects of annosus root disease on large or small trees on various habitat types.

RRTYPE--Specifies the root disease type to be simulated. -We specified the "*Armillaria* type" and then modified it for this exercise.

SAREA--Specifies the stand area to be simulated and recalculates the linear dimension for the stand. In the Western Root Disease Model, all stands are assumed to be square.

SPREAD--Specifies the type of root disease spread routine to be simulated. The dynamic

[3] WP-white pine; WL=western larch; DF-Douglas-fir; TF-grand fir or white fir; C-cedar; LP-lodgepole pine; ES-Engelmann spruce; PP-ponderosa pine

spread routine was used in this exercise.

TDISIN--Describes the type of tree distribution in the stand. A random distribution was assumed for the simulations of root disease.

TTDMULT--Changes the time-to-death multipliers for mortality caused by root disease. The multipliers permit the user to vary the time-to-death by site and tree species. Values were set by tree species as follows for this exercise:

WP	WL	DF	TF	C	LP	ES	PP[3]
10.0	2.0	2.0	.75	2.0	2.0	2.0	10.0

STREAD--Although this Keyword was not used directly in these simulations it is important to understand its use because it may be useful in future modeling of annosus root disease. The Keyword is used to initialize stumps within root diseased areas of the stand. These stumps serve as inoculum sources from which infection spreads during the simulation. No parameter fields are read in conjunction with this Keyword. The user, however, is expected to supply records that contain the necessary stump information.

Stumps are defined as any infected trees that are killed by any means. The tree can be a stump formed by cutting, a dead standing tree, or a tree which has been snapped off by wind. The important attribute of these stumps is that they represent trees infected by root disease, regardless of how they actually died. We did not use this Keyword because we worked strictly with area in root disease (RRINIT), not specific pieces of inoculum.

DESCRIPTION OF SIMULATIONS FOR ANNOSUS ROOT DISEASE

The following simulations (runs) were made to provide some output from the Western Root Disease Model, as modified to represent annosus root disease, and to indicate the effects of various management alternatives.

RUN1A (Base run with under- and overstory removal):
- Under- and overstory removal (all stems < 1 inch and $\geq$ 17 inches DBH) in year 1987
- Run with no further stand entry until year 2107; assume no root disease

RUN1B (Base run with a clearcut and planting with ponderosa pine):
- Clearcut in year 1987
- Planted with ponderosa pine (PP), 305 stems per acre, in year 1988
- No root disease; continue the simulation until year 2107

RUN1C (Same as RUN1B, except planted with white fir)

RUN2A (Base run with under- and overstory removal and two thinnings from above):
- Under- and overstory removal (all stems < 1 inch and $\geq$ 17 inches DBH) in year 1987
- Thin from above in year 2027 to remove 20 percent of existing Basal Area
- Thin from above in year 2057 to remove 20 percent of existing Basal Area
- Assume no root disease; continue simulation until year 2107

RUN2B (Disease run, no control operations):
Under- and overstory removal (all stems < 1 inch and $\geq$ 17 inches DBH) in year 1987
- Root disease present on 3.28 acres, 70 centers. No "jump" after cut; INOCSPAN, INFKILL, INFMULT, and TTDMULT as prescribed for *H. annosum* on this site.
- Thin from above in year 2027 to remove 20 percent of existing Basal Area. RRJUMP set at 0.5 to add about 4 acres to the root disease area at thinning.
- Thin from above in year 2057 to remove 20 percent of existing Basal Area. RRJUMP set at same rate as in year 2027 to increase root disease area at thinning.
- Continue simulation until year 2107

RUN3A (Disease run with no thinning):
- Under- and overstory removal (all stems < 1 inch and $\geq$ 17 inches DBH) in year 1987
- Root disease present on 3.28 acres, 70 centers. INOCSPAN, INFKILL, INFMULT, and TTDMULT set as prescribed for *H. annosum* on this site.
- No thinning; continue simulation until year 2107

RUN4A (Simulated control at both thinnings, but not during overstory removal):
- Under- and overstory removal (all stems 1 inch and $\geq$ 17 inches DBH) in year 1987
- Root disease present on 3.28 acres, 70 centers. INOCSPAN, INFKILL, INFMULT, and TTDMULT set as prescribed for *H. annosum* on this site.
- In year 2027 thin from above to remove 20 percent of existing Basal Area. RRJUMP set at 0.0 to simulate control.
- In year 2057 thin from above to remove 20 percent of existing Basal Area. RRJUMP set at 0.0 to simulate control.
- Continue simulation until year 2107

RUN4B (Bark Beetle attack in year 2027):
- Under- and overstory removal (all stems < 1 inch and $\geq$ 17 inches DBH) in year 1987
- Root disease present on 3.28 acres, 70 centers. INOCSPAN, INFKILL, INFMULT, and TTDMULT set as prescribed for *H. annosum* on this site.
- BBTYPE3 invoked in year 2027 on white fir: minimum DBH, 10 inches; minimum

- density, five trees per acre; mortality rate of 0.88; and 0.30 as the minimum level of root infection necessary for eligibility for bark beetle attack.
- Continue simulation until year 2107

RUN6B (Same as RUN2B, but with a moderate preference for removal of PP during thinning)

RESULTS AND DISCUSSION

Figure 4 depicts timber volumes after 120 years, including timber recovered by thinning, that were predicted by the various simulations. As seen in Run 2A, the site would be reasonably productive (93,763 board feet per acre) with proper management and no root disease. The difference in volumes predicted by the clearcut and plant options (Runs 1C and 1B), indicates that the site, in the absence of root disease, is better suited to growing white fir (total recoverable volume of 85,312 board feet per acre) than ponderosa pine (72,398 board feet per acre). In fact, without root disease, planting ponderosa pine (RUN 1B; 72,398 board feet per acre) would be a less desirable alternative than an overstory removal in 1987 followed by no further management (Run 1A; 80,696 board feet per acre).

The reality of root disease markedly alters the desirability of many of these alternatives. For example, with root disease the no-management option (RUN 3A) produces substantially less volume (57,283 board feet per acre) than the option to clear-cut and plant ponderosa pine (RUN 1B; 72,398 board feet per acre). The thinning that looked so desirable in the absence of root disease (RUN 2A; 93,763 board feet per acre) becomes a questionable alternative as recoverable volume shrinks considerably (RUN 2B, 61,687 board feet per acre).

Interestingly, results from RUN 4A (66,331 board feet per acre) suggest that control through stump treatment at both thinnings is only marginally beneficial--most likely because root disease became established throughout the stand during the 1987 overstory removal. If thinning favors removal of ponderosa pine, which is disease resistant on this site (an action we believe timber managers may invoke to "sweeten the pot" to attract bids on the thinning sale), then the effects of root disease are further exacerbated (RUN 6B; 56,260 board feet per acre).

The effect of an attack by bark beetles (RUN 4B; 53,468 board feet per acre) reduced volumes less than anticipated (compare to RUN 3A; 57,283 board feet per acre), probably because most

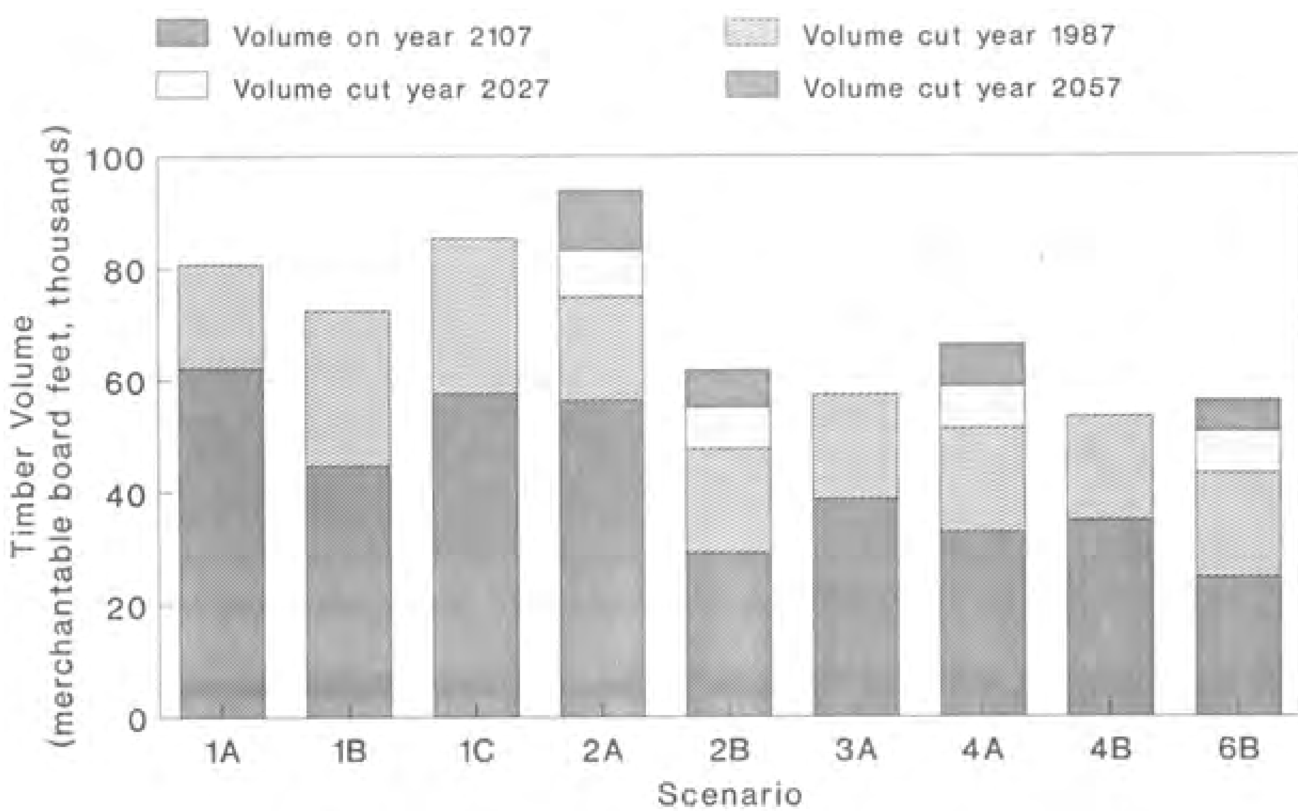

Figure 4--Projected merchantable timber volumes for the nine simulations made with the experimental annosus variant of the Western Root Disease Model.

trees killed by bark beetles eventually would have died from root disease. Whether this simulation actually portrays effects of an endemic rather than an epidemic level of bark beetles is certainly open to discussion, as are the criteria we set to invoke the attack. Interestingly, more stringent criteria did not allow the attack to occur at all.

Figure 5 provides a temporal view of the area encompassed by root disease. Regardless of what management actions were invoked, the stand area occupied by root disease was rather constant with only stump treatment showing a slight reduction. This result suggests that, based on the assumptions we made, any scenario that leaves white fir in the stand without treatment of stumps at the initial entry (the 1987 overstory removal in this case) will lead to development of severe disease conditions within the planned 120-yr rotation.

CONCLUSIONS AND CONCERNS

We believe this exercise clearly demonstrates that the Western Root Disease Model has considerable potential, primarily through its User-Controlled Keyword System, for adaptation to represent effects of annosus root disease in the coniferous forests of western North America. We say this with full recognition that data sets are not available to evaluate the accuracy of these simulations. Our experience, however, suggests they are reasonable and provide a useable estimate of what could occur if the various management actions were implemented.

Surely many problems and concerns exist. Nevertheless, we believe this paper provides a suitable base from which to develop a model for evaluating alternative management scenarios in affected stands and to help develop forest plans in areas impacted by annosus root disease. Before assuming that this little exercise has solved all the problems, however, we urge you to consider the following questions:

1. Where, when, and how will we get data sets to evaluate the accuracy of these simulations?
2. Are our epidemiological assumptions reasonable for other geographic areas?
3. What about stands in which pine alone, or both pine and white fir, are affected by annosus root disease?
4. How variable are disease dynamics by location, habitat, fungal type, etc.?
5. What other Keywords might be useful?
6. What data sets are available to help justify modification of model equations?
7. Is critical epidemiological information missing? If so, how do we obtain it?

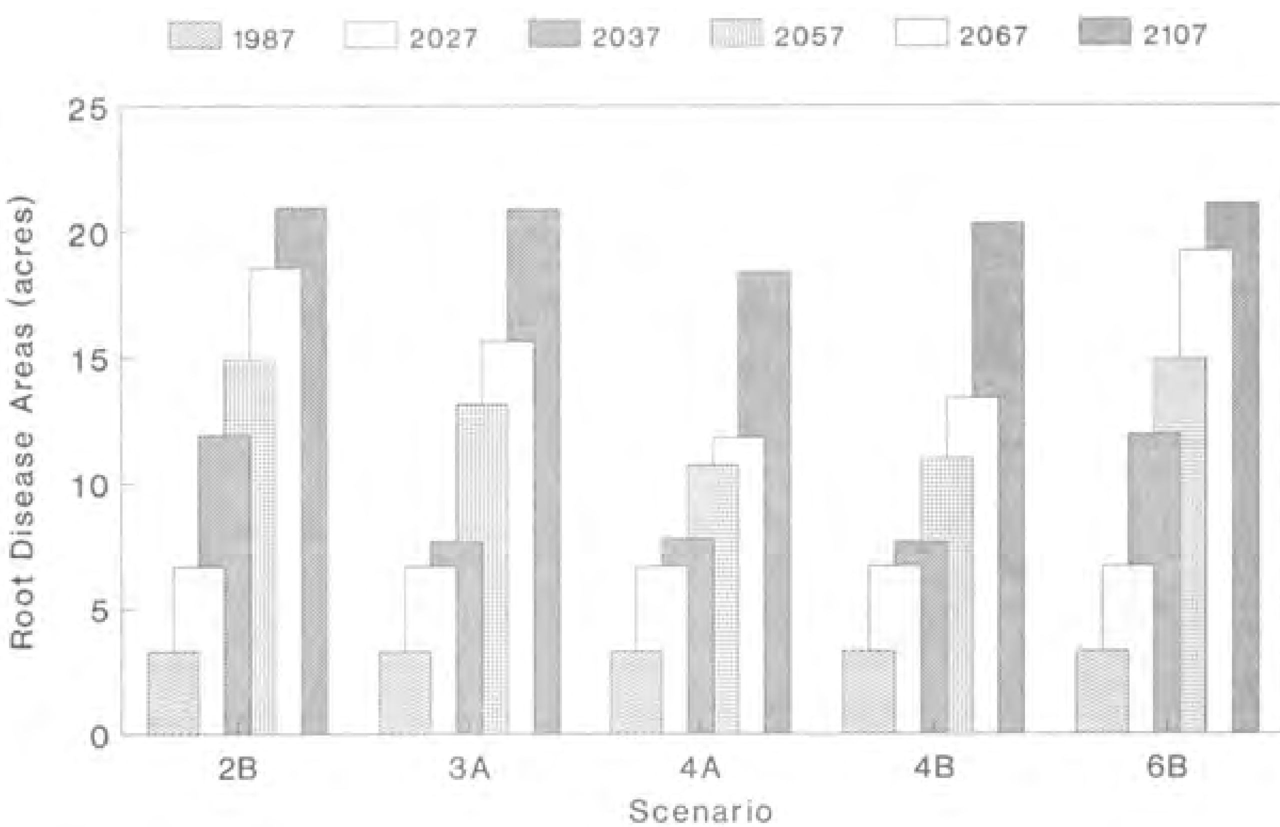

Figure 5--Projected acres of root disease area for the nine simulations made with this experimental annosus variant of the Western Root Disease Model.

8. Is the interaction with bark beetles adequately captured by the model?
9. Will forest managers find the model useful and use it as a tool?
10. How costly will it be to develop an annosus root disease model as an on-line, functional entity, and who (or what agency) should be responsible for doing so?
11. Can the Prognosis model's program be changed to allow the base Prognosis model to be stopped and restarted during a simulation to enter additional disease information?
12. Is stump treatment with borax during intermediate stand entries a more effective control than these simulations suggest ?

These currently unanswered questions are posed to stimulate interest and to suggest paths of investigation. We believe this paper provides a viable beginning for a model that, with further development, can help forest pathologists and forest managers understand and control annosus root disease in the coniferous forests of western North America.

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